

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/249,671A

D.F. 3/4/96 #13
 CRF Processing Date: 3/4/96
 Edited by: [Signature]
 Verified by: [Signature] (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other **ENTERED**
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 16:50:20

INPUT SET: S9110.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANTS: Hauptmann, R.
Falkner, E.
Bodo, G.
VoÄ, T.
Maurer-Fogy, I.

(ii) TITLE OF INVENTION: Process for Preparing and Purifying
alpha-Interferon

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
(B) STREET: 1100 New York Avenue, Suite 600
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/249,671
(B) FILING DATE: 26-MAY-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0652.1350000

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 371-2600
(B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO: 1:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 16:50:24

INPUT SET: S9110.raw

47
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 25 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: both
52 (D) TOPOLOGY: unknown
53
54 (ii) MOLECULE TYPE: cDNA
55
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
57
58 CGTCTTCAAG AATTGAGAT TATCG 25
59
60 (2) INFORMATION FOR SEQ ID NO: 2:
61
62 (i) SEQUENCE CHARACTERISTICS:
63 (A) LENGTH: 56 base pairs
64 (B) TYPE: nucleic acid
65 (C) STRANDEDNESS: both
66 (D) TOPOLOGY: unknown
67
68 (ii) MOLECULE TYPE: cDNA
69
70
71
72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
73
74 GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCTTAA ACTTTC 56
75
76 (2) INFORMATION FOR SEQ ID NO: 3:
77
78 (i) SEQUENCE CHARACTERISTICS:
79 (A) LENGTH: 35 base pairs
80 (B) TYPE: nucleic acid
81 (C) STRANDEDNESS: both
82 (D) TOPOLOGY: unknown
83
84 (ii) MOLECULE TYPE: cDNA
85
86
87
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89
90 ATGCCTATGC ATGTGATCTG CCTCAAACCC ACAGC 35
91
92 (2) INFORMATION FOR SEQ ID NO: 4:
93
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH: 34 base pairs
96 (B) TYPE: nucleic acid
97 (C) STRANDEDNESS: both
98 (D) TOPOLOGY: unknown
99

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

DATE: 03/04/96
TIME: 16:50:30

INPUT SET: S9110.raw

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152

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGCAGATCAC ATGCATAGGC ATTTGTAGCA ATAG

34

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30

Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145 150 155 160

Leu Arg Ser Lys Glu
165

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

 DATE: 03/04/96
 TIME: 16:50:33

INPUT SET: S9110.raw

153

154

(2) INFORMATION FOR SEQ ID NO: 6:

155

156

(i) SEQUENCE CHARACTERISTICS:

157

(A) LENGTH: 495 base pairs

158

(B) TYPE: nucleic acid

159

(C) STRANDEDNESS: both

160

(D) TOPOLOGY: unknown

161

162

(ii) MOLECULE TYPE: cDNA

163

164

165

(ix) FEATURE:

166

(A) NAME/KEY: CDS

167

(B) LOCATION: 1..495

168

169

170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

171

172

TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG 48

173

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met

174

1 5 10 15

175

176

CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC 96

177

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp

178

20 25 30

179

180

AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA 144

181

Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln

182

35 40 45

183

184

AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC 192

185

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe

186

50 55 60

187

188

AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC 240

189

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu

190

65 70 75 80

191

192

CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA 288

193

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu

194

85 90 95

195

196

GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG 336

197

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys

198

100 105 110

199

200

GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC 384

201

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu

202

115 120 125

203

204

TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA 432

205

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

 DATE: 03/04/96
 TIME: 16:50:37

INPUT SET: S9110.raw

206	130	135	140	
207				
208	GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT	480		
209	Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser			
210	145 150 155 160			
211				
212	TTA AGA AGT AAG GAA	495		
213	Leu Arg Ser Lys Glu			
214	165			
215				
216				
217				
218	(2) INFORMATION FOR SEQ ID NO: 7:			
219				
220	(i) SEQUENCE CHARACTERISTICS:			
221	(A) LENGTH: 869 base pairs			
222	(B) TYPE: nucleic acid			
223	(C) STRANDEDNESS: both			
224	(D) TOPOLOGY: unknown			
225				
226	(ii) MOLECULE TYPE: cDNA			
227				
228				
229				
230	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:			
231				
232	GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAATGA CCAACAGCGG	60		
233				
234	TTGATTGATC AGGTAGAGGG GGCCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC	120		
235				
236	GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA	180		
237				
238	AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTACCG CCGAGACTTA TAGTCGCTTT	240		
239				
240	GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC	300		
241				
242	GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT	360		
243				
244	CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG	420		
245				
246	AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG	480		
247				
248	TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG	540		
249				
250	ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC	600		
251				
252	AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG	660		
253				
254	GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC	720		
255				
256	TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT	780		
257				
258	GTCAGAGCAG AAATCATGAG ATCTTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA	840		

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:01

INPUT SET: S9110.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANTS: Hauptmann, R.
Falkner, E.
Bodo, G.
VoÄ, T.
Maurer-Fogy, I.

(ii) TITLE OF INVENTION: Process for Preparing and Purifying
alpha-Interferon

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
(B) STREET: 1100 New York Avenue, Suite 600
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/249,671
(B) FILING DATE: 26-MAY-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0652.1350000

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 371-2600
(B) TELEFAX: (202) 371-2540

unhappy test
Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

 DATE: 03/04/96
 TIME: 15:06:03

INPUT SET: S9110.raw

ERRORED SEQUENCES FOLLOW:

154 (2) INFORMATION FOR SEQ ID NO: 6:

155

156

(i) SEQUENCE CHARACTERISTICS:

157

(A) LENGTH: 495 base pairs

158

(B) TYPE: nucleic acid

159

(C) STRANDEDNESS: both

160

(D) TOPOLOGY: unknown

161

162

(ii) MOLECULE TYPE: cDNA

163

164

165

(ix) FEATURE:

166

(A) NAME/KEY: CDS

167

(B) LOCATION: 1..495

168

169

170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

171

172

TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG

173

48

174

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met

175

1

5

10

15

176

177

CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC

178

96

179

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp

180

20

25

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181

182

AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA

183

144

184

Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln

185

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186

187

AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC

188

192

189

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe

190

50

55

60

191

192

AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC

193

240

194

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu

195

65

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196

197

CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA

198

288

199

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu

200

85

90

95

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:05

INPUT SET: S9110.raw

201
202 GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG
203 336
204 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
205 100 105 110
206
207 GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC
208 384
209 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
210 115 120 125
211
212 TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA
213 432
214 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
215 130 135 140
216
217 GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT
218 480
219 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
220 145 150 155 160
221
222 TTA AGA AGT AAG GAA
223 495
224 Leu Arg Ser Lys Glu
225 165
226
227
228

229 (2) INFORMATION FOR SEQ ID NO: 7:
230

231 (i) SEQUENCE CHARACTERISTICS:

232 (A) LENGTH: 869 base pairs

233 (B) TYPE: nucleic acid

234 (C) STRANDEDNESS: both

235 (D) TOPOLOGY: unknown
236237 (ii) MOLECULE TYPE: cDNA
238
239
240241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
242243 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAATGA CCAACAGCGG
244 60
245246 TTGATTGATC AGGTAGAGGG GGCCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC
247 120
248249 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
250 180
251

252 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTACCGG CCGAGACTTA TAGTCGCTTT

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:07

INPUT SET: S9110.raw

253 240
254
255 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTTATGAA AAAGAATATC
256 300
257
258 GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT
259 360
260
261 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG
262 420
263
264 AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG
265 480
266
267 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG
268 540
269
270 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC
271 600
272
273 AAATCTTACA CTGAACCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG
274 660
275
276 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC
277 720
278
279 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT
280 780
281
282 GTCAGAGCAG AAATCATGAG ATCTTTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA
283 840
284
285 AGTAAGGAAT GATAACGATC GTAACCTGCA
286 869
287

288 (2) INFORMATION FOR SEQ ID NO: 8:
289

290 (i) SEQUENCE CHARACTERISTICS:

- > 291 (A) LENGTH: 1177 base pairs
292 (B) TYPE: nucleic acid
293 (C) STRANDEDNESS: both
294 (D) TOPOLOGY: unknown

295
296 (ii) MOLECULE TYPE: cDNA
297

298
299 (ix) FEATURE:

- 300 (A) NAME/KEY: CDS
301 (B) LOCATION: 286..873
302 (D) OTHER INFORMATION: /function= "Cytokine"
303 /product= "Interferon-omega1"
304

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:09

INPUT SET: S9110.raw

305 (ix) FEATURE:
306 (A) NAME/KEY: mat_peptide
307 (B) LOCATION: 355..873
308 (D) OTHER INFORMATION: /function= "Cytokine"
309 /product= "Interferon-omega"
310
311 (ix) FEATURE:
312 (A) NAME/KEY: sig_peptide
313 (B) LOCATION: 286..354
314 (D) OTHER INFORMATION: /product= "ST II Leader"
315
316 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
317
318 GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAATGA CCAACAGCGG
319 60
320
321 TTGATTGATC AGGTAGAGGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC
322 120
323
324 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
325 180
326
327 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTACGG CCGAGACTTA TAGTCGCTTT
328 240
329
330 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTT ATG AAA AAG
331 294
332 Met Lys Lys
333 -23
334
335 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
336 342
337 Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
338 -20 -15 -10 -5
339
340 AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG
341 390
342 Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg
343 1 5 10
344
345 AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG
346 438
347 Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu
348 15 20 25
349
350 TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA
351 486
352 Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys
353 30 35 40
354
355 GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG
356 534
357 Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

 DATE: 03/04/96
 TIME: 15:06:12

INPUT SET: S9110.raw

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358				
359				
360	CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT GCT GCC			
361	582			
362	Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala			
363	65	70	75	
364				
365	TGG AAC ATG ACC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT CAG CAA			
366	630			
367	Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln			
368	80	85	90	
369				
370	CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTA GTG GGA GAA GGA GAA			
371	678			
372	Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu			
373	95	100	105	
374				
375	TCT GCT GGG GCA ATT AGC AGC CCT GCA CTG ACC TTG AGG AGG TAC TTC			
376	726			
377	Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe			
378	110	115	120	
379				
380	CAG GGA ATC CGT GTC TAC CTG AAA GAG AAG AAA TAC AGC GAC TGT GCC			
381	774			
382	Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala			
383	125	130	135	140
384				
385	TGG GAA GTT GTC AGA ATG GAA ATC ATG AAA TCC TTG TTC TTA TCA ACA			
386	822			
387	Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr			
388	145	150	155	
389				
390	AAC ATG CAA GAA AGA CTG AGA AGT AAA GAT AGA GAC CTG GGC TCA TCT			
391	870			
392	Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser			
393	160	165	170	
394				
395	TGAAATGATT CTCATTGATT AATTTGCCAT ATAACACTTG CACATGTGAC TCTGGTCAAT			
396	930			
397				
398	TCAAAAGACT CTTATTTTCGG CTTTAATCAC AGAATTGACT GAATTAGTTC TGCAAATACT			
399	990			
400				
401	TTGTCGGTAT ATTAAGCCAG TATATGTTAA AAAGACTTAG GTTCAGGGGC ATCAGTCCCT			
402	1050			
403				
404	AAGATGTTAT TTATTTTAC TCATTTATTT ATTCTTACAT TTTATCATAT TTATACTATT			
405	1110			
406				
407	TATATTCTTA TATAACAAAT GTTTGCCTTT ACATTGTATT AAGATAACAA AACATGTTCA			
408	1170			
409				
410	GGATCCA			

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:14

INPUT SET: S9110.raw

411 1177
412
413

464 (2) INFORMATION FOR SEQ ID NO: 10:

465

466

(i) SEQUENCE CHARACTERISTICS:

467

(A) LENGTH: 879 base pairs

468

(B) TYPE: nucleic acid

469

(C) STRANDEDNESS: both

470

(D) TOPOLOGY: unknown

471

472

(ii) MOLECULE TYPE: cDNA

473

474

475

476

(ix) FEATURE:

477

(A) NAME/KEY: CDS

478

(B) LOCATION: 286..852

479

480

(ix) FEATURE:

481

(A) NAME/KEY: mat_peptide

482

(B) LOCATION: 355..852

483

(D) OTHER INFORMATION: /function= "Cytokine"

484

/product= "Interferon-alpha-2c"

485

486

(ix) FEATURE:

487

(A) NAME/KEY: sig_peptide

488

(B) LOCATION: 286..354

489

(D) OTHER INFORMATION: /product= "ST II Leader"

490

491

492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

493

494

GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG

495

60

496

497

TTGATTGATC AGGTAGAGGG GGCCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC

498

120

499

500

GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA

501

180

502

503

AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT

504

240

505

506

GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTT ATG AAA AAG

507

294

508

Met Lys Lys

509

-23

510

511

AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA

512

342

RAW SEQUENCE LISTING PATENT APPLICATION *US/08/249,671A*

 DATE: 03/04/96
 TIME: 15:06:16

INPUT SET: S9110.raw

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513   Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
514   -20                               -15                     -10                -5
515
516   AAT GCC TAT GCA TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG
517   390
518   Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg
519               1                               5                 10
520
521   AGG ACC TTG ATG CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC
522   438
523   Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser
524               15                               20                 25
525
526   TGC TTG AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC
527   486
528   Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly
529               30                               35                 40
530
531   AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC
532   534
533   Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile
534               45                               50                 55                60
535
536   CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG
537   582
538   Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp
539               65                               70                 75
540
541   GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG
542   630
543   Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu
544               80                               85                 90
545
546   AAT GAC CTG GAA GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT
547   678
548   Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr
549               95                               100                105
550
551   CCC CTG ATG AAG GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA
552   726
553   Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln
554               110                               115                120
555
556
557
558   AGA ATC ACT CTC TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG
559   774
560   Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp
561   125                               130                 135                140
562
563   GAG GTT GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC
564   822
565   Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn
    
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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:18

INPUT SET: S9110.raw

566		145		150		155
567						
568	TTG CAA GAA AGT TTA AGA AGT AAG GAA TGATAACGAT CGTAACTGCA					
569	869					
570	Leu Gln Glu Ser Leu Arg Ser Lys Glu					
571		160		165		
572						
573	GAAGCTTAAT					
574	879					
575						

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:19*INPUT SET: S9110.raw*

Line	Error	Original Text
157	Entered (495) and Calc. Seq. Length (0) differ	(A) LENGTH: 495 base pairs
232	Entered (869) and Calc. Seq. Length (0) differ	(A) LENGTH: 869 base pairs
291	Entered (1177) and Calc. Seq. Length (0) differ	(A) LENGTH: 1177 base pairs
467	Entered (879) and Calc. Seq. Length (0) differ	(A) LENGTH: 879 base pairs